FIG. 1A

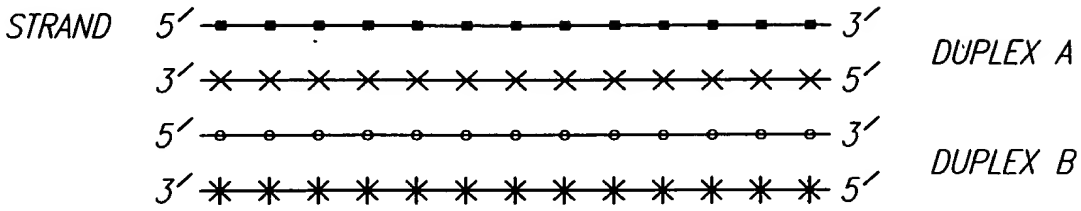


FIG. 1B

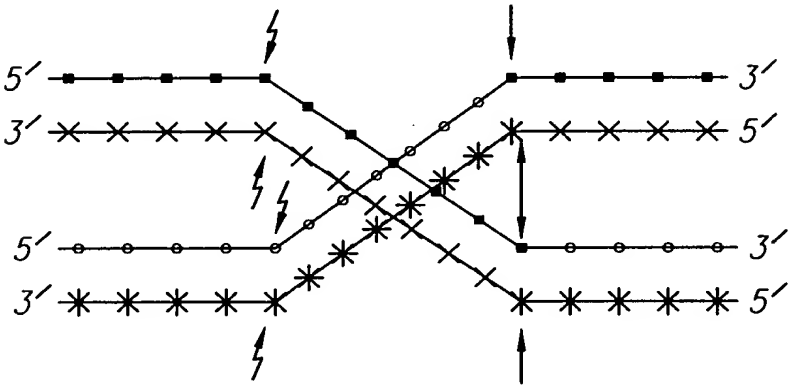
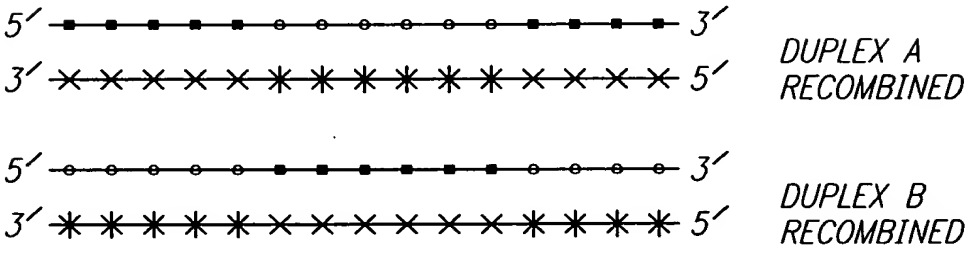


FIG. 1C



- ▪ 5′ TO 3′ DNA SEGMENT 1
- × 3′ TO 5′ DNA SEGMENT 1

> DUPLEX A

- ∘ 5′ TO 3′ DNA SEGMENT 2
- ✳ 3′ TO 5′ DNA SEGMENT 2

> DUPLEX B

↓ STRAND BREAK + LIGATION

↯ CUT SITE + LIGATION

FIG. 2

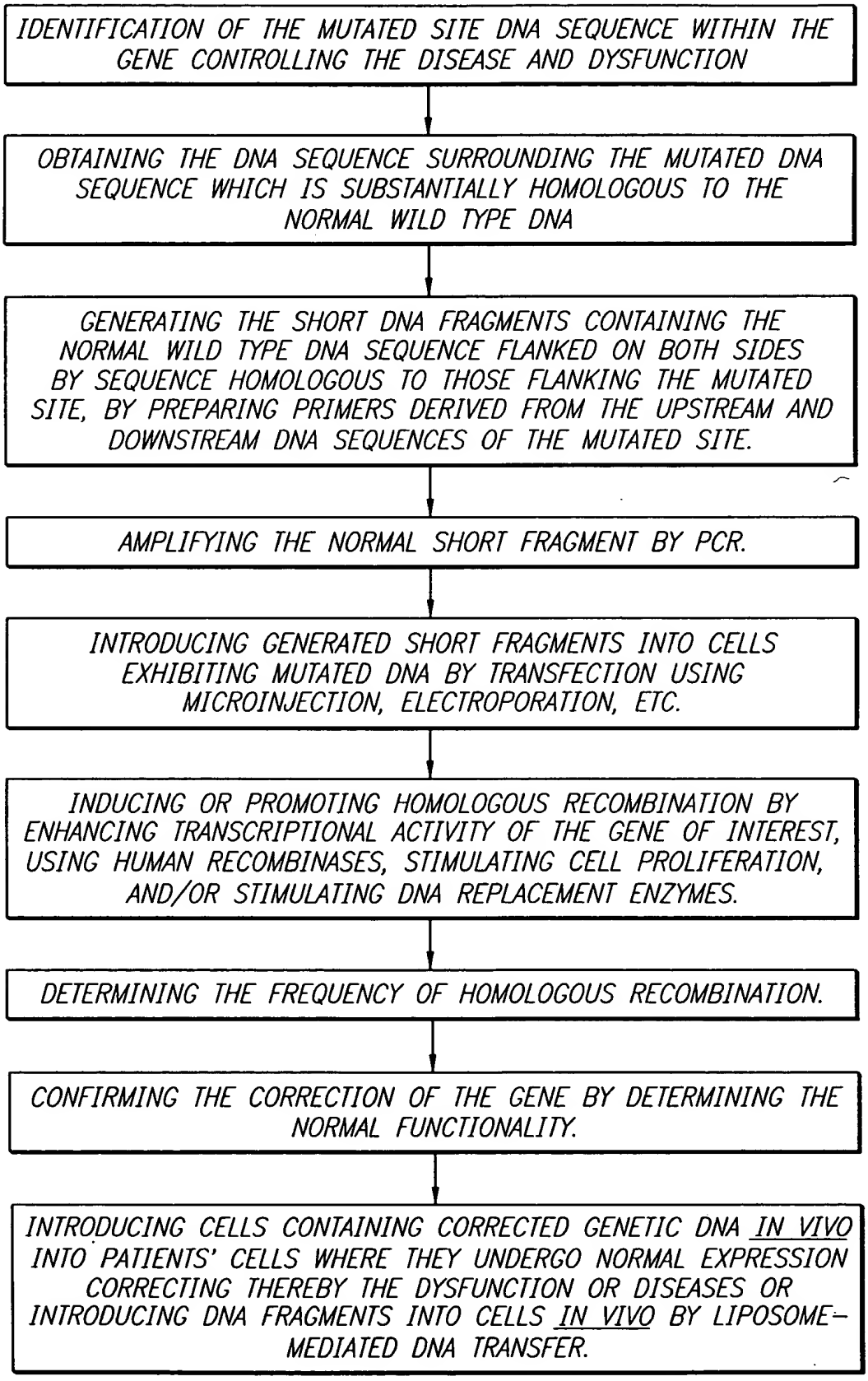
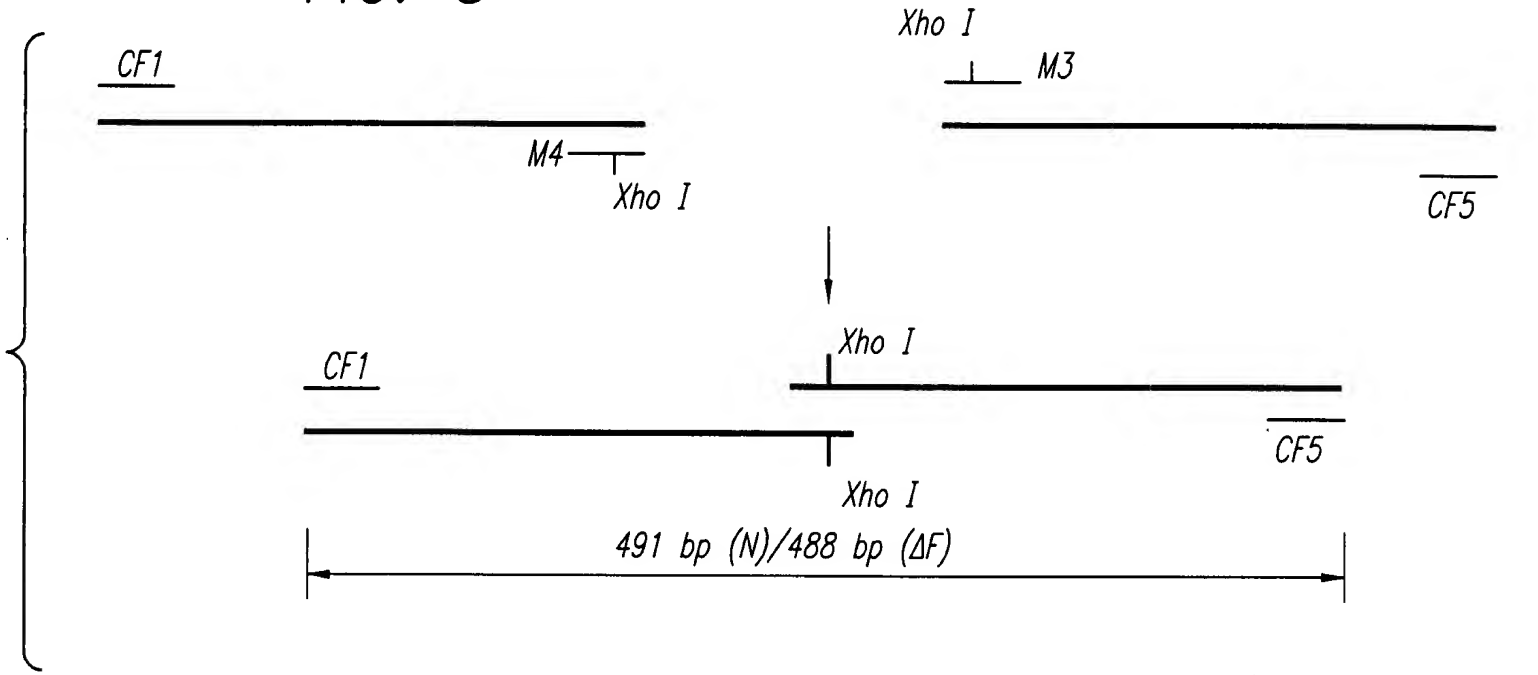


FIG. 3



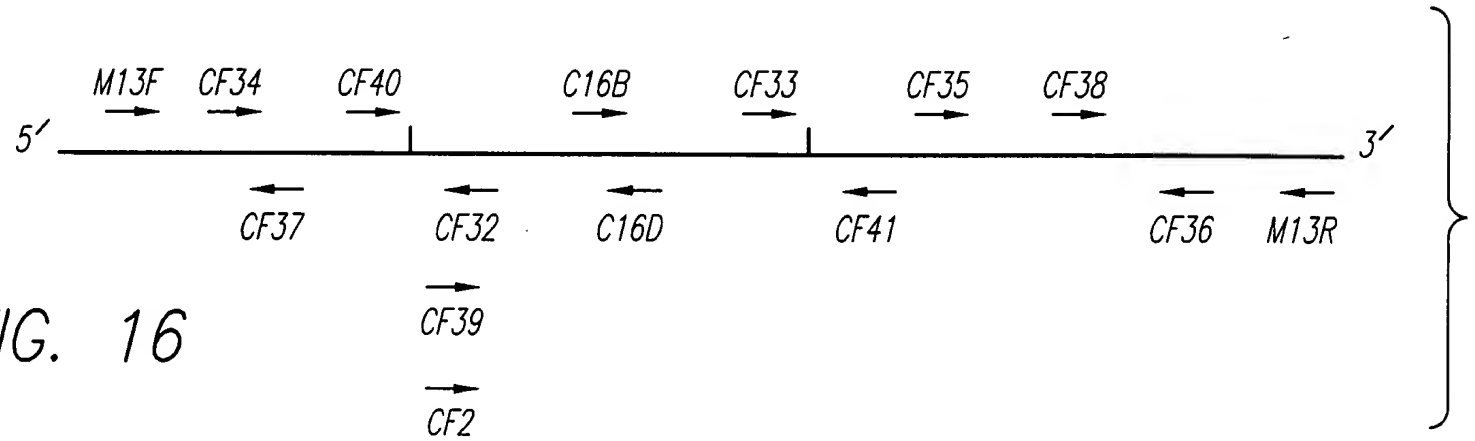


FIG. 16

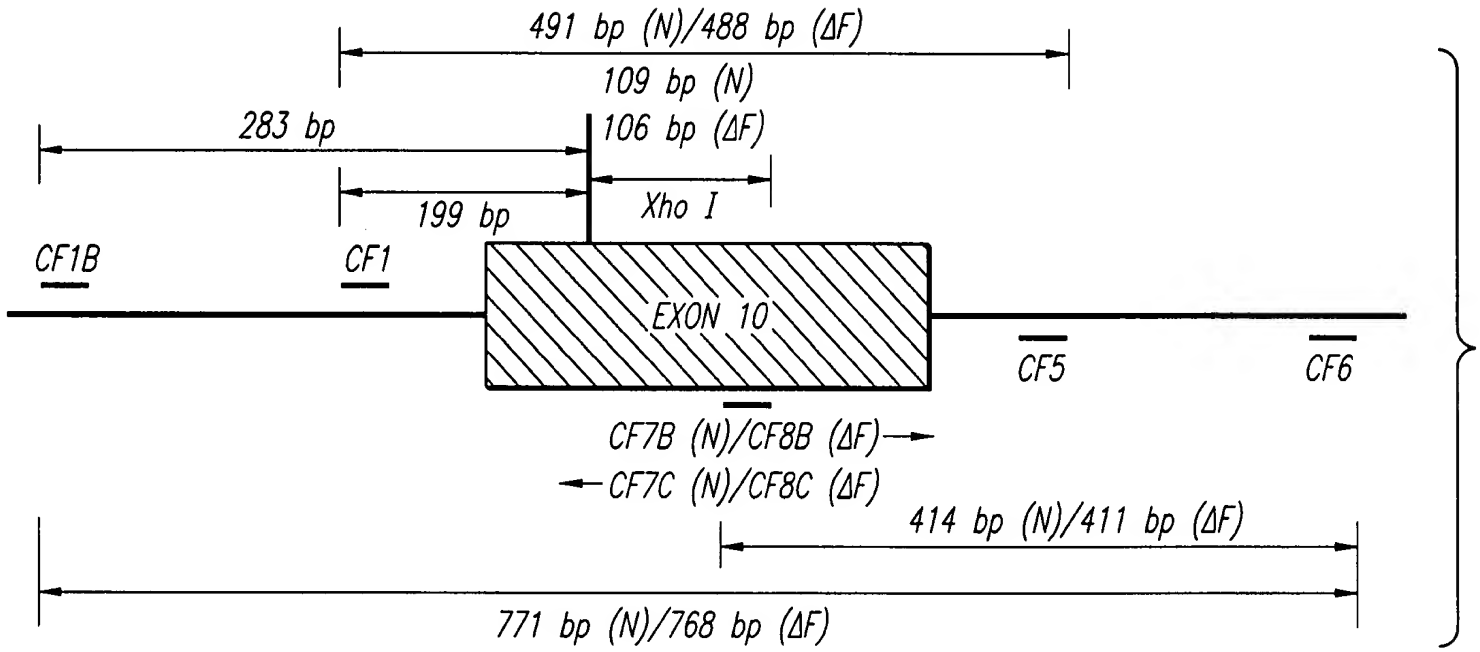


FIG. 4

FIG. 5

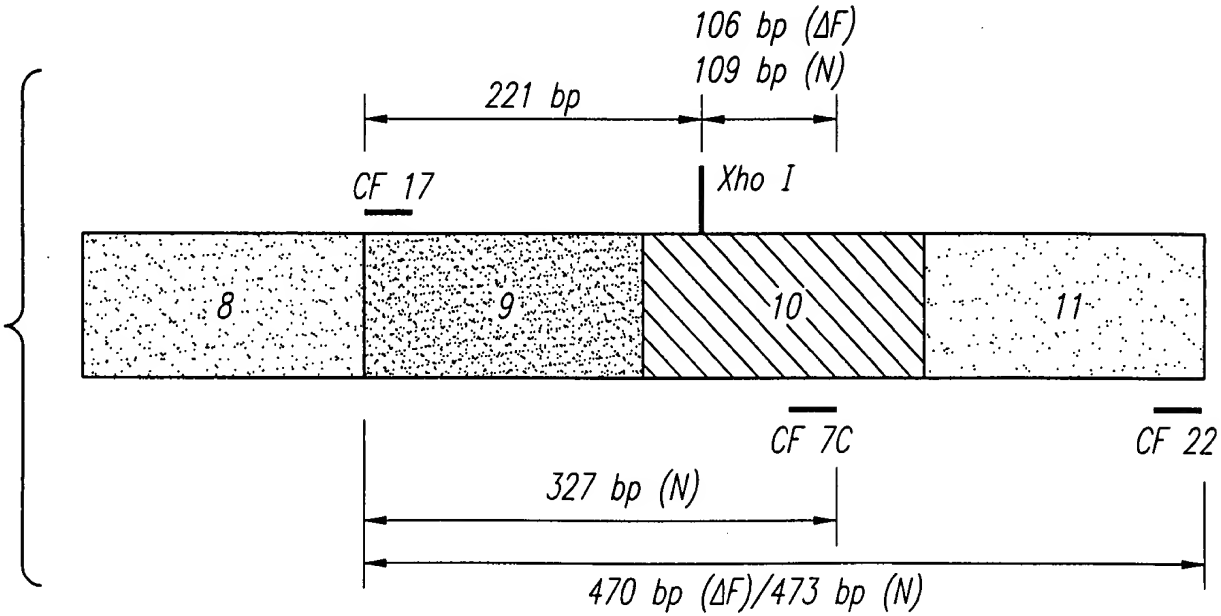


FIG. 6A

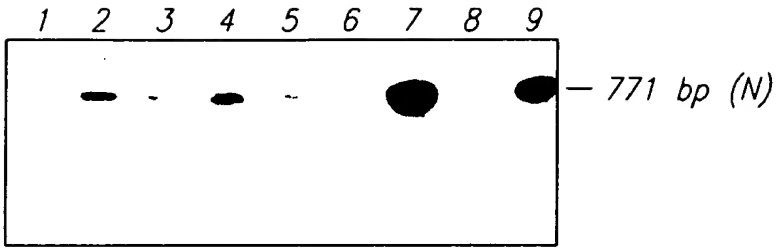


FIG. 6B

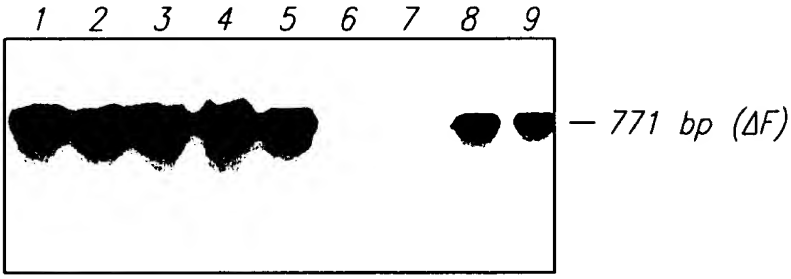


FIG. 7A

FIG. 7B

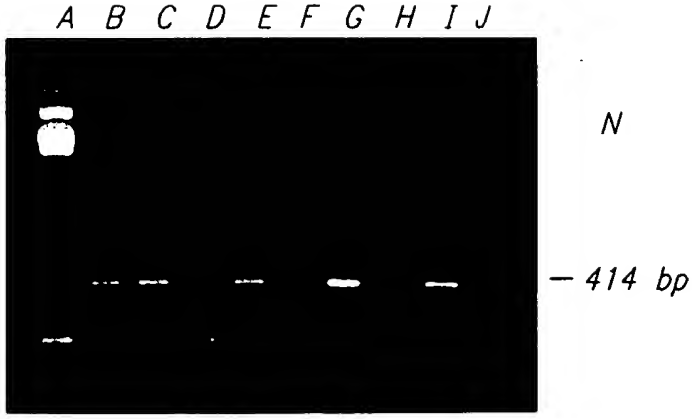


FIG. 8A

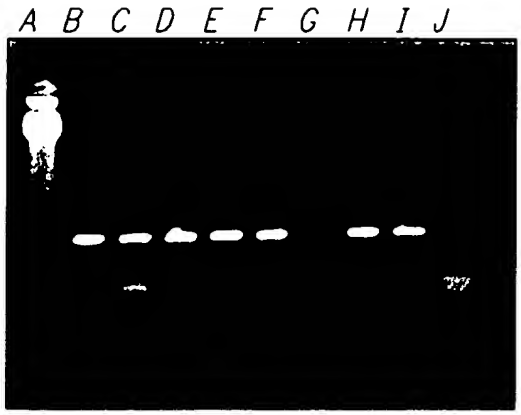
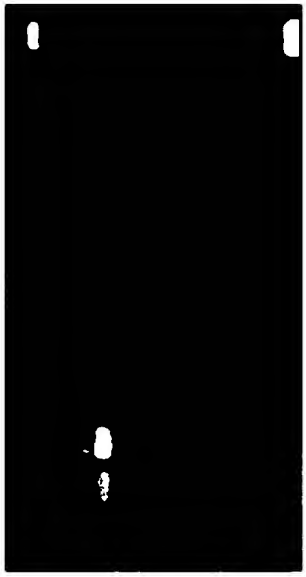


FIG. 8B

FIG. 9



123 BP marker
1:1000000; CF7B
1:100000; CF7B
1:10000; CF7B
1:1000; CF7B
1:100; CF7B
1:10; CF7B
1:1; CF7B
1:0.1; CF7B
1:1000000; CF8B; CFPAC
1:1000000; CF7B; 16HBE
1:1000000; CF7B; water

FIG. 10

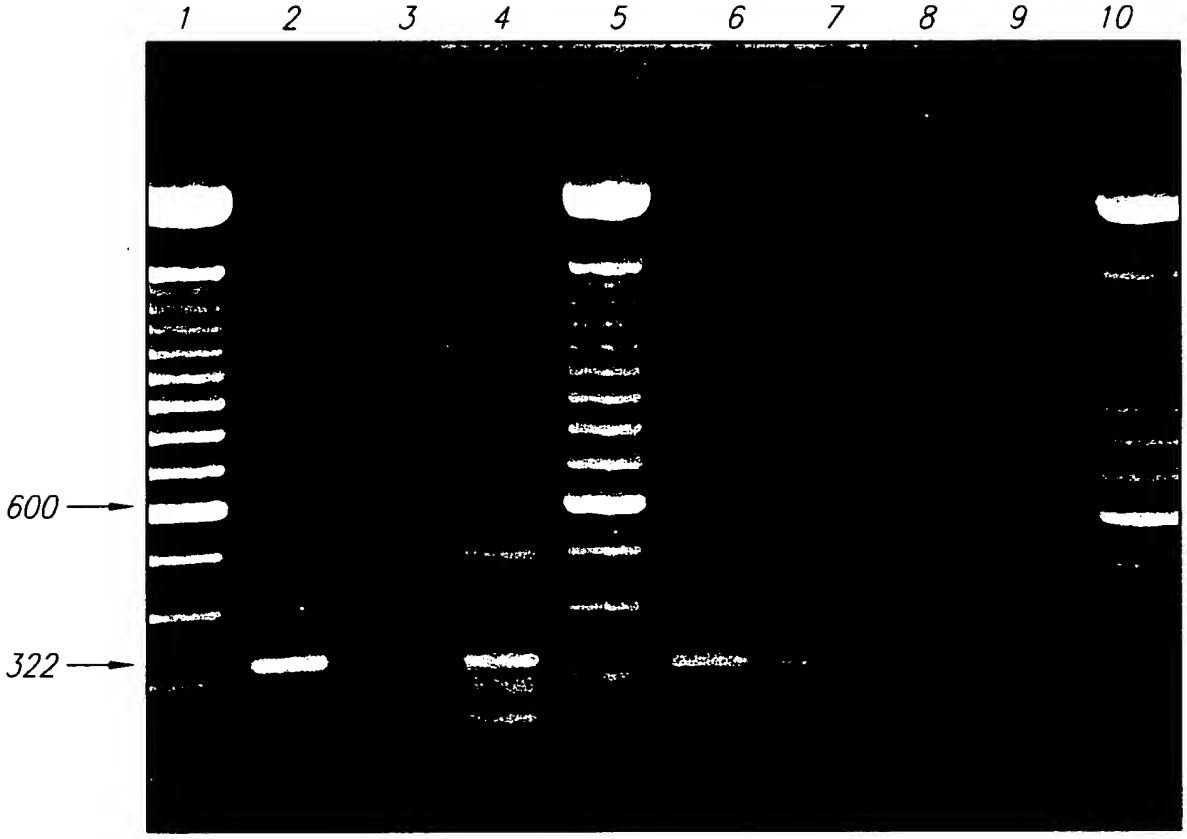


FIG. 11

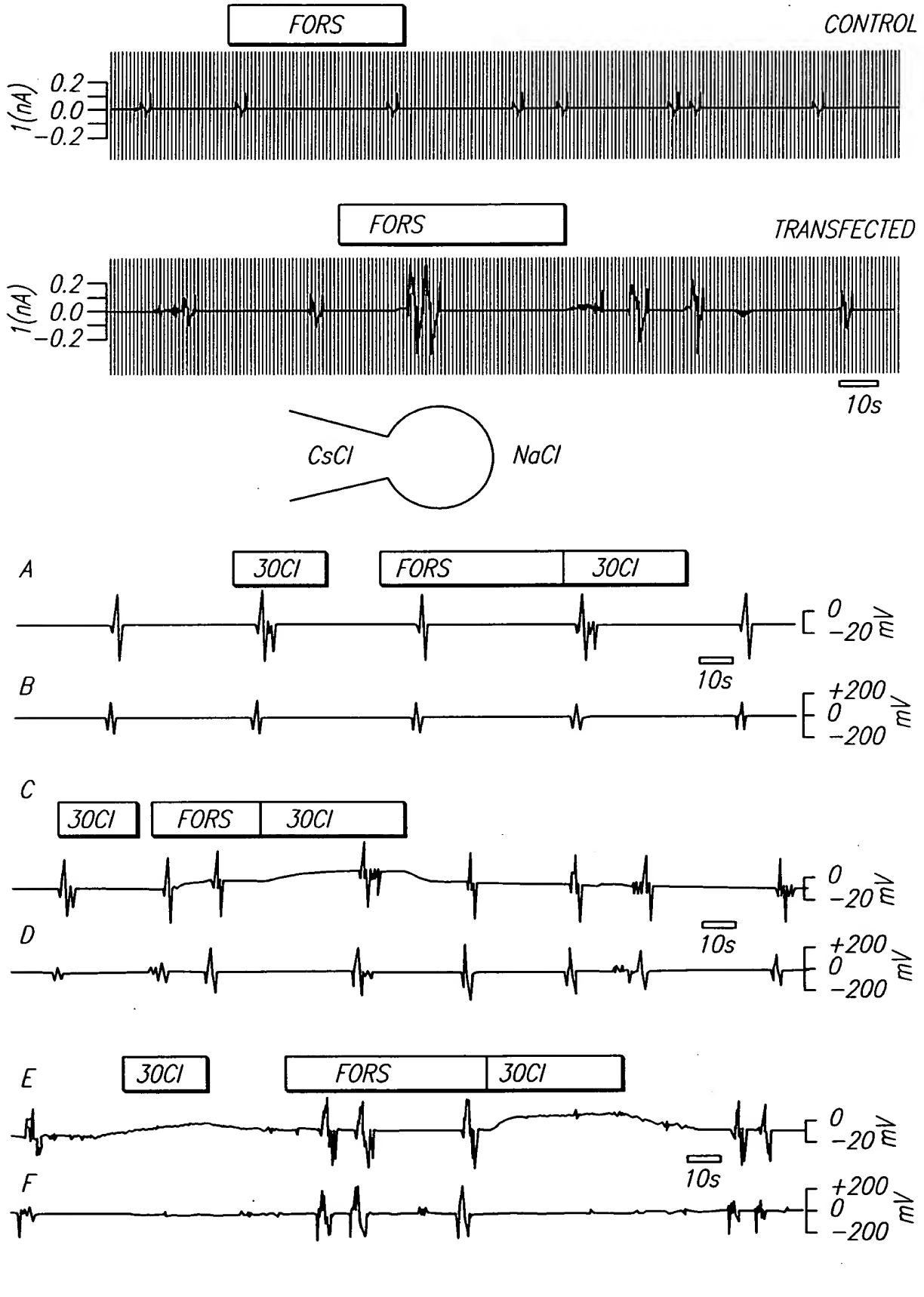


FIG. 12

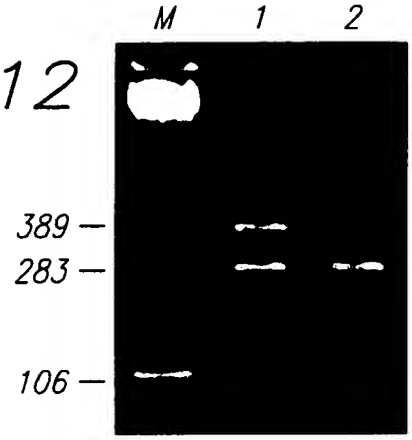


FIG. 13

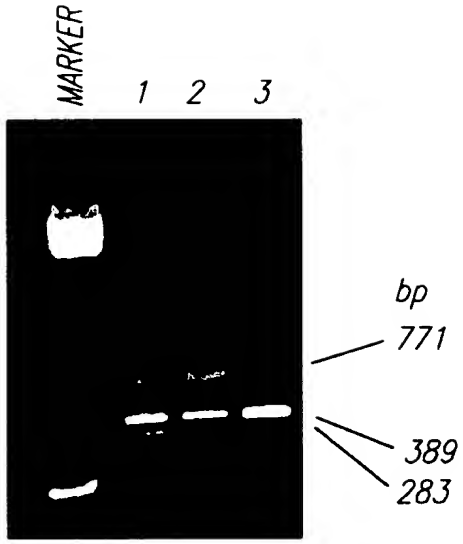


FIG. 14

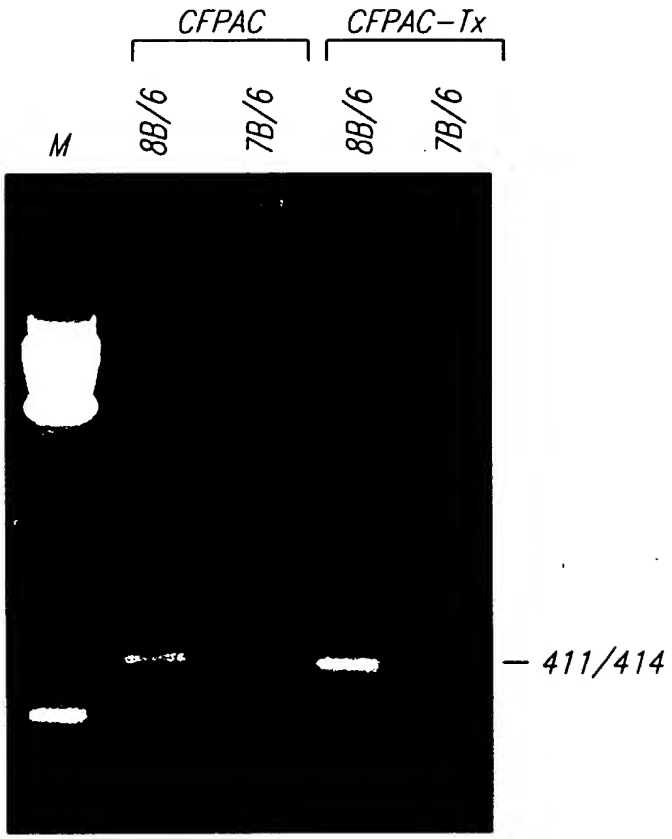


FIG. 15

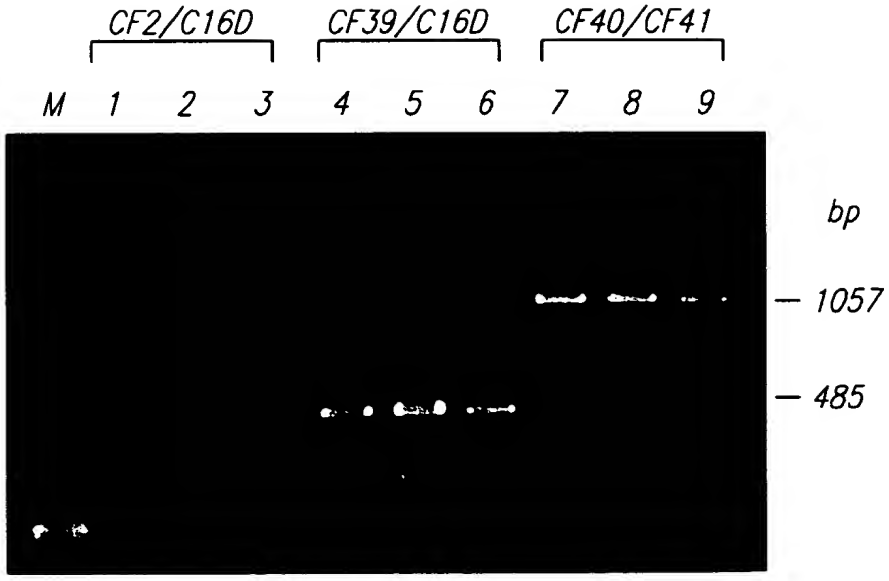
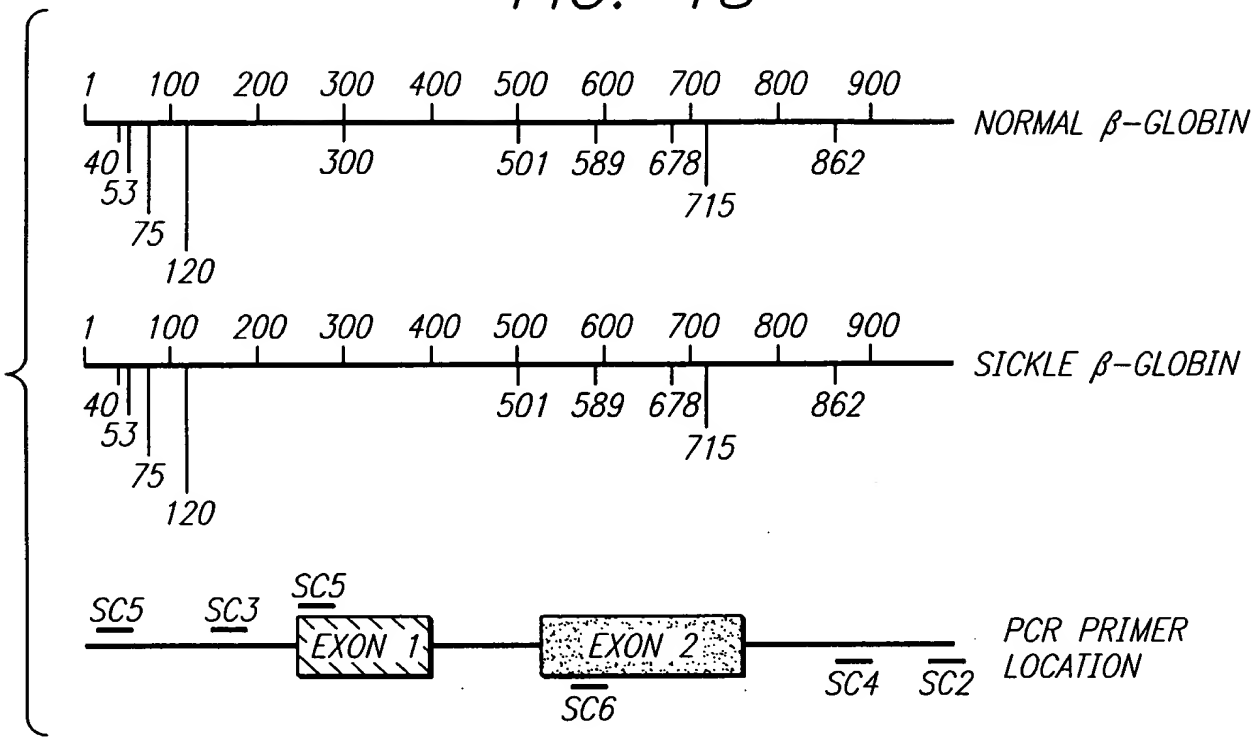


FIG. 17

FIG. 18



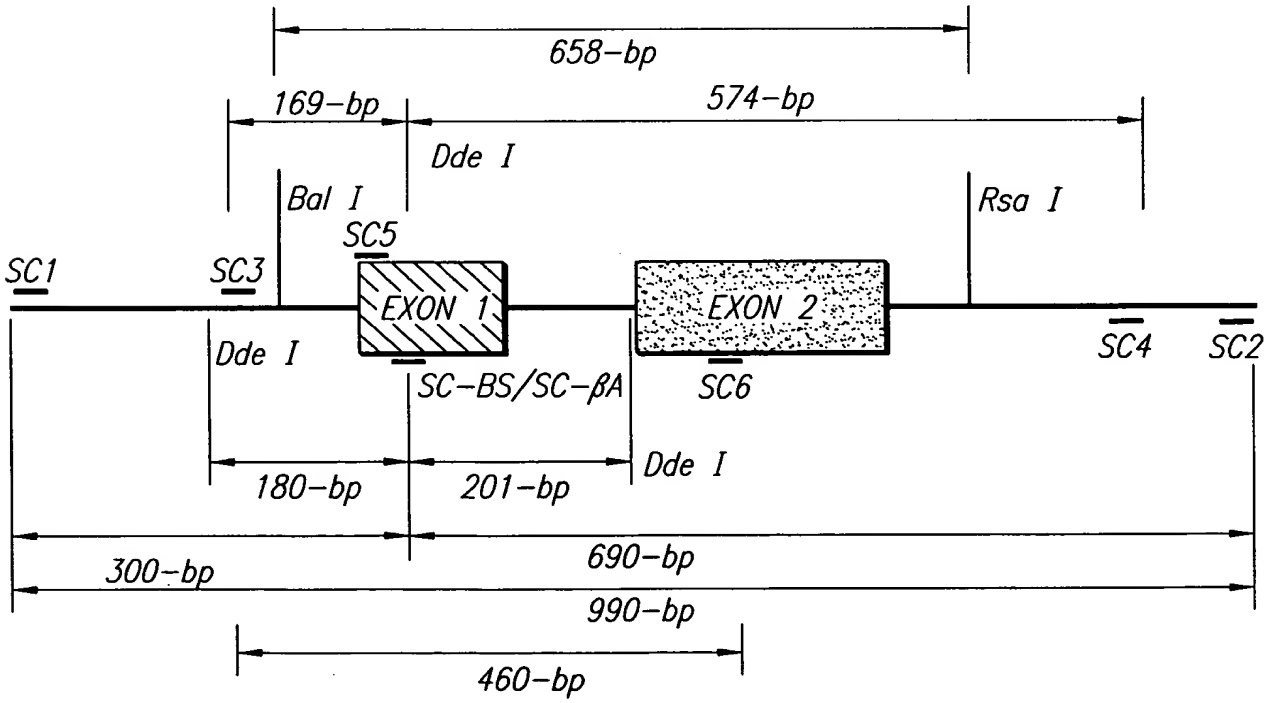
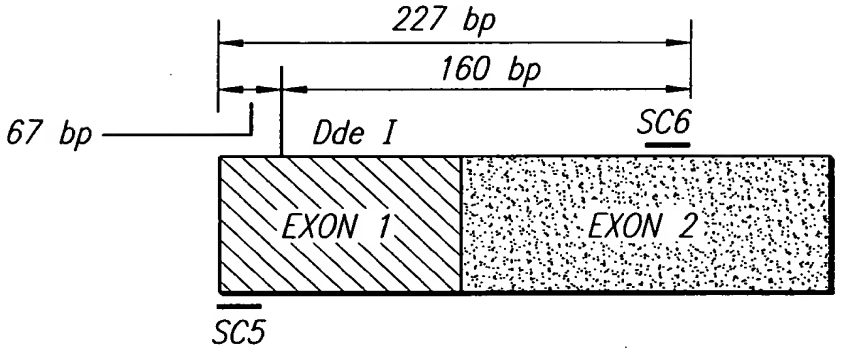


FIG. 19

FIG. 20



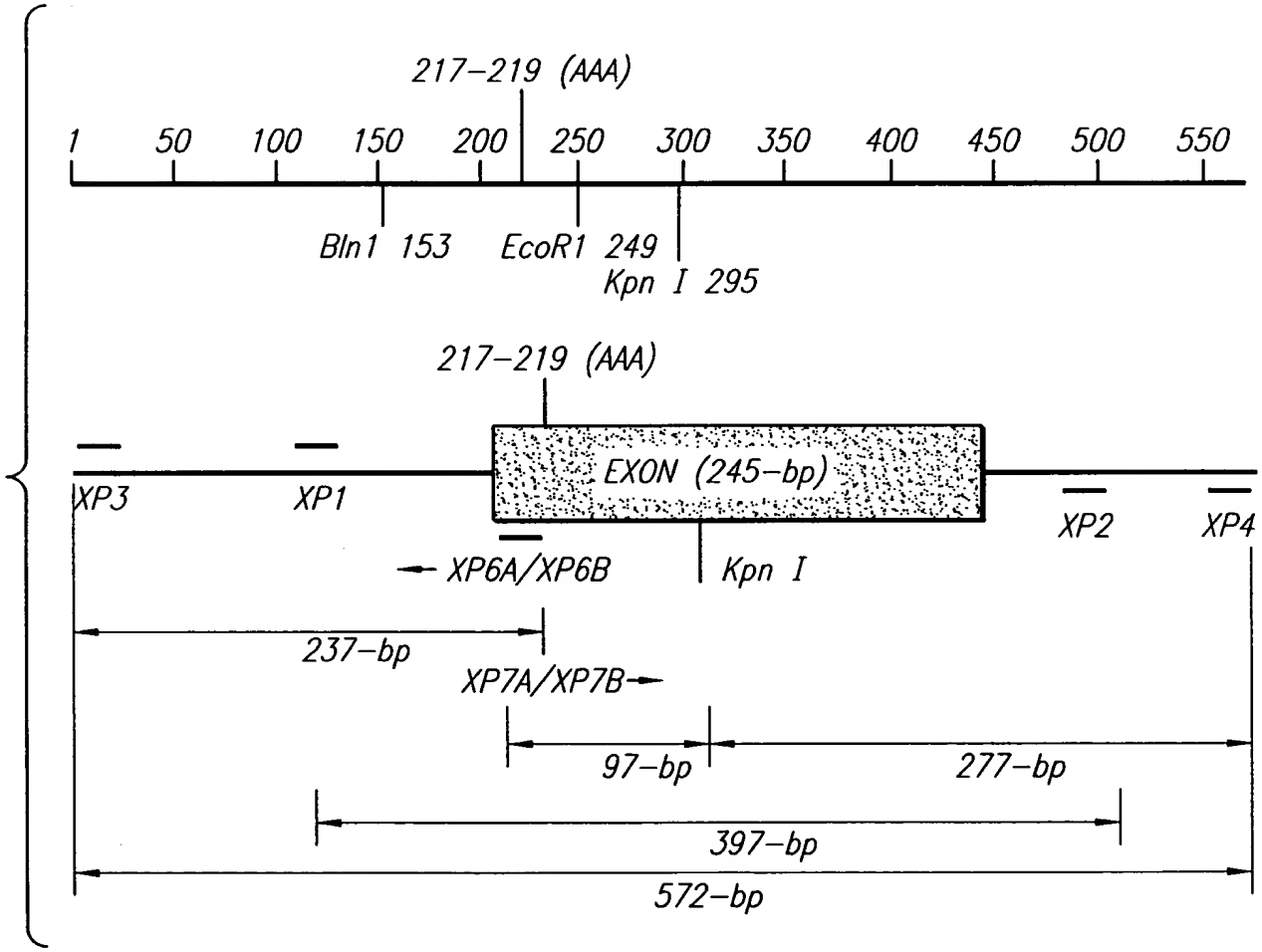
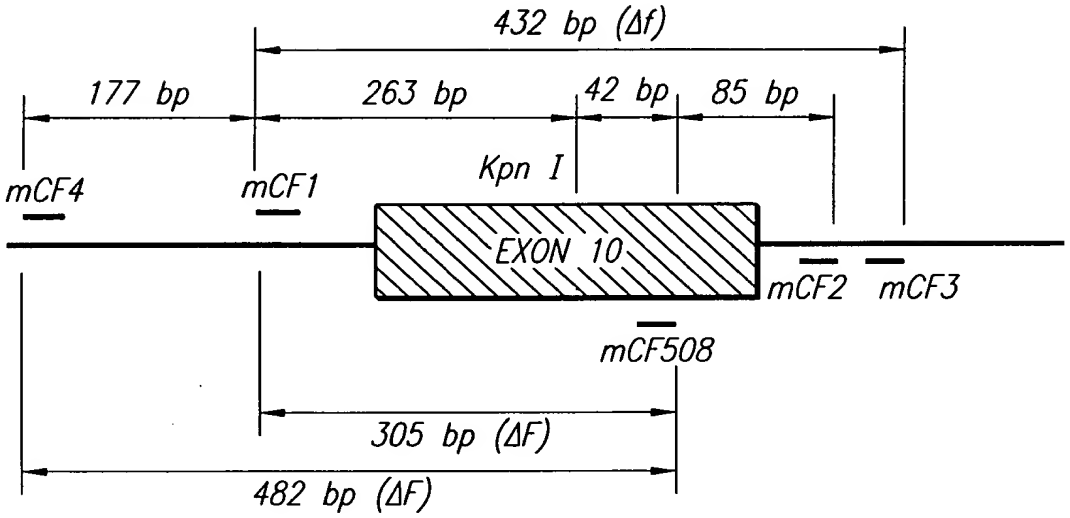


FIG. 21

FIG. 22



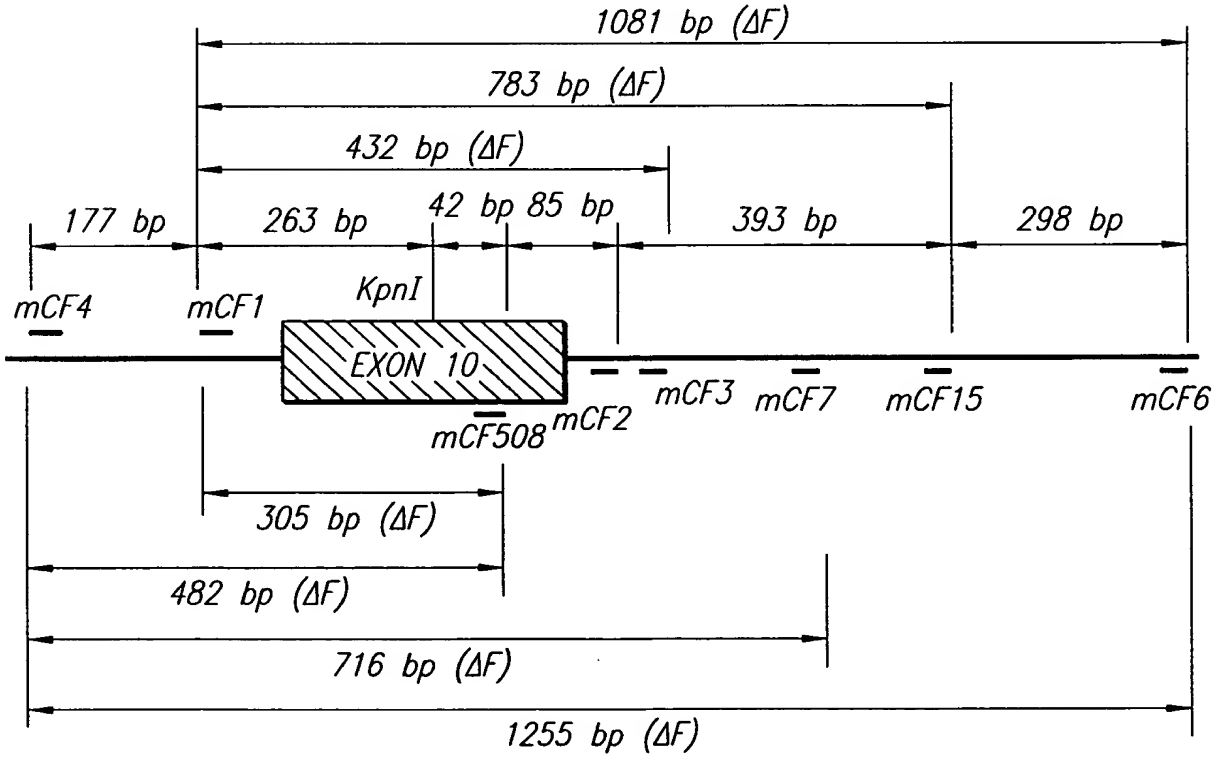


FIG. 23

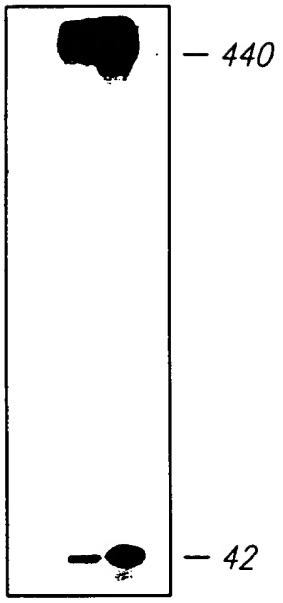


FIG. 24

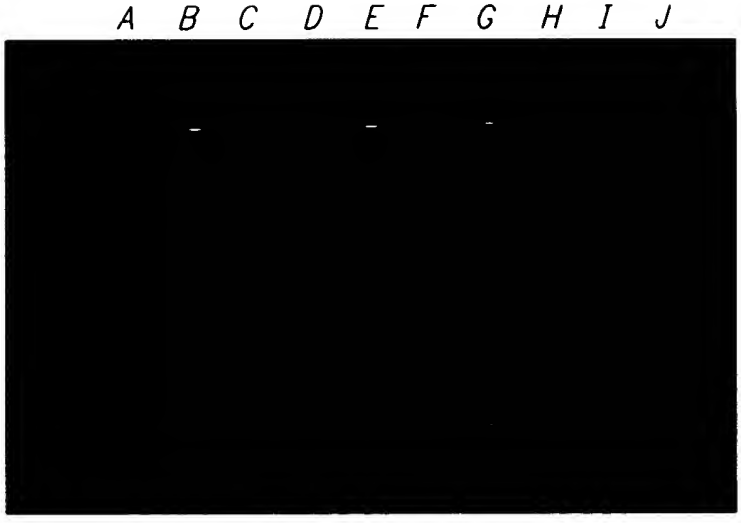


FIG. 25

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

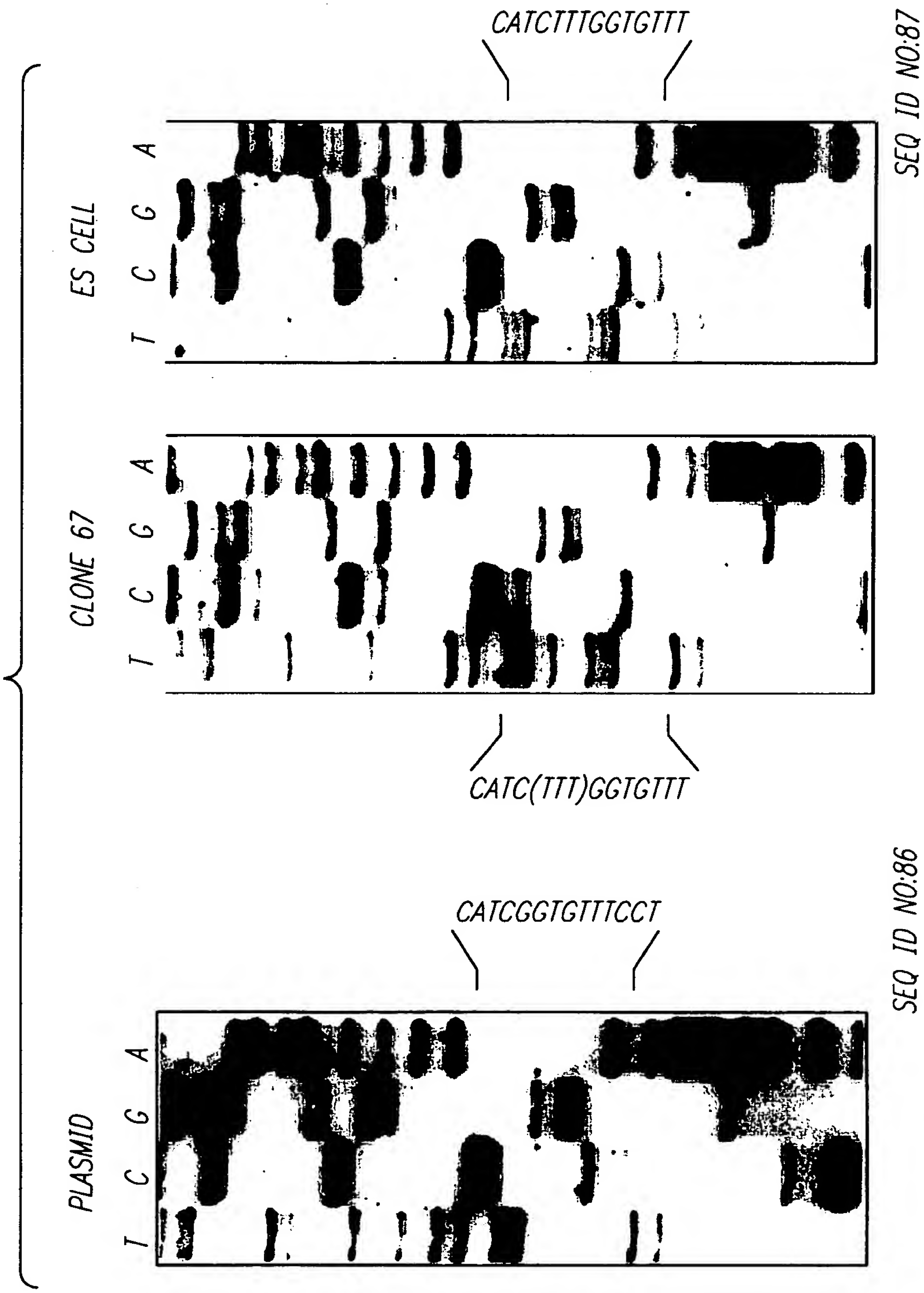


FIG. 26

FIG. 27

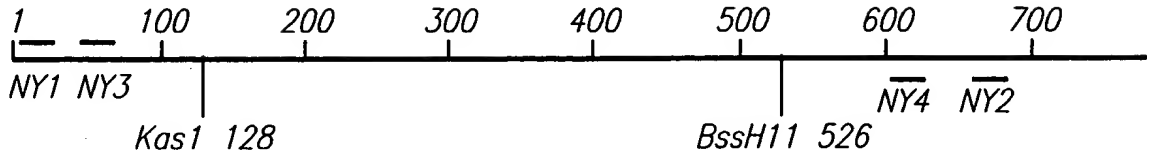
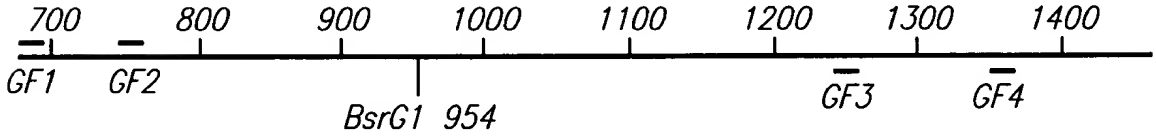


FIG. 28



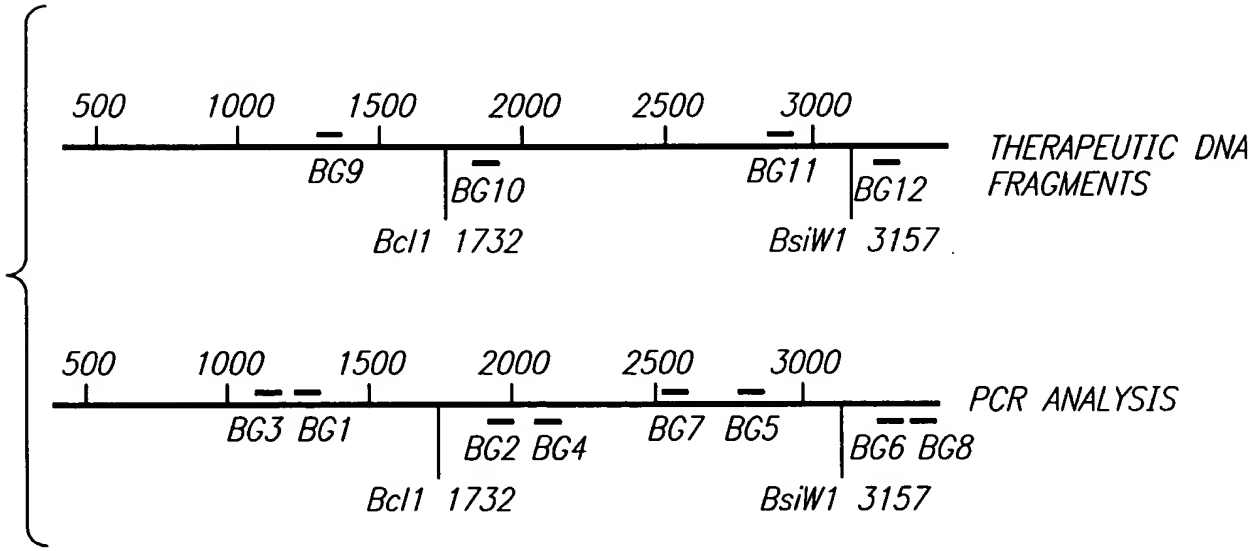


FIG. 29

FIG. 30A

```
GAATTCCAGC CAGACGTGAT GGCGGGTGCC CGTAGTCCCA GCTACTCGGG AGGCTGAGGC     60
AGGAGAATGG CGTGAACCCA GGAGGCAGAA CTTGCAGTGA GCCGAGATCG CGCCACTGCA    120
CTCTAGCCTG GGTGACAGAG TGAGACTCTG TCTCTAAATA AATAAATAAA TAAATAAATA    180
AATAAATAAA ATCAGTGCTT TTTCTTCCTC TGCTACCTCC TTTCCTTCTA CTCAGTTTTA    240
GTCAGTAGTA TTATCTTTTT TCAGATTTAT CTTTGTATTG TTAAATCTGC TTATGCTTCT    300
ATTACTTTAT TTATTAGCTT TAAATGATAC CTTTTGACTT TCAGCTTTTC TTAATAAAGC    360
AATCAGCAAA TTTCCTTTAC ACTCCACACT TATACCCCAT TTCCTTTGTT TGTTTATTTG    420
GTTTTTACTT CTAACTTTTC TTATTGTCAG GACATATAAC ATATTTAAAC TTTGTTTTTC    480
AACTCGAATT CTGCCATTAG TTTTAATTTT TGTTCACAGT TATATAAATC TTTGTTCACT    540
GATAGTCCTT TTGTACTATC ATCTCTTAAA TGACTTTATA CTCCAAGAAA GGCTCATGGG    600
AACAATATTA CCTGAATATG TCTCTATTAC TTAATCTGTA CCTAATAATA TGAAGGTAAT    660
CTACTTTGTA GGATTTCTGT GAAGATTAAA TAAATTAATA TAGTTAAAGC ACATAGAACA    720
GCACTCGACA CAGAGTGAGC ACTTGGCAAC TGTTAGCTGT TACTAACCTT TCCCATTCTT    780
                                    cactgtagct gtactacctt ccat
CCTCCAAACC TATTCCAACT ATCTGAATCA TGTGCCCCTT CTCTGTGAAC CTCTATCATA    840
ctcctc.... .......... .......... .......-.. .......... ..........
ATACTTGTCA CACTGTATTG TAATTGTCTC TTTTACTTTC CCTTGTATCT TTTGTGCATA    900
.......... .......... .......... .......... .......... ..........
GCAGAGTACC TGAAACAGGA AGTATTTTAA ATATTTTGAA TCAAATGAGT TAATAGAATC    960
.......... .......... .......... .......... .......... ..........
TTTACAAATA AGAATATACA CTTCTGCTTA GGATGATAAT TGGAGGCAAG TGAATCCTGA   1020
.......... .......... .......... .......... .......... ..........
GCGTGATTTG ATAATGACCT AATAATGATG GGTTTTATTT CCAGACTTCA CTTCTAATGA   1080
.......... .......... .......... .......... .......... ..........
TGATTATGGG AGAACTGGAG CCTTCAGAGG GTAAAATTAA GCACAGTGGA AGAATTTCAT   1140
.......... .......... .......... .......... .......... ..........
TCTGTTCTCA GTTTTCCTGG ATTATGCCTG GCACCATTAA AGAAAATATC ATCTTTGGTG   1200
.......... .......... .......... .......... .......... ..........
TTTCCTATGA TGAATATAGA TACAGAAGCG TCATCAAAGC ATGCCAACTA GAAGAGGTAA   1260
.......... .......... .......... .......... .......... ..........
GAAACTATGT GAAAACTTTT TGATTATGCA TATGAACCCT TCACACTACC CAAATTATAT   1320
.......... .......... .......... .......... .......... ..........
ATTTGGCTCC ATATTCAATC GGTTAGTCTA CATATATTTA TGTTTCCTCT ATGGGTAAGC   1380
.......... .......... .......... .......... .......... ..........
TACTGTGAAT GGATCAATTA ATAAAACACA TGACCTATGC TTTAAGAAGC TTGCAAACAC   1440
.......... .......... .......... .......... .......... ..........
ATGAAATAAA TGCAATTTAT TTTTTAAATA ATGGGTTCAT TTGATCACAA TAAATGCATT   1500
.......... .......... .......... .......... .......... ..........
TTATGAAATG GTGAGAATTT TGTTCACTCA TTAGTGAGAC AAACGTCCTC AATGGTTATT   1560
.......... .......... .......... .......... .......-.. ..........
TATATGGCAT GCATATAAGT GATATGTGGT ATCTTTTTAA AAGATACCAC AAAATATGCA   1620
.......... .......-.. ..........
TCTTTAAAAA TATACTCCAA AAATTATTAA GATTATTTTA ATAATTTTAA TAATACTATA   1680
GCCTAATGGA ATGAGCATTG ATCTGCCAGC AGAGAATTAG AGGGGTAAAA TTGTGAAGAT   1740
ATTGTATCCC TGGCTTTGAA CAAATACCAT ATAACTTCTA GTGACTGCAA TTCTTTGATG   1800
CAGAGGCAAA ATGAAGATGA TGTCATTACT CATTTCACAA CAATATTGGA GAATGAGCTA   1860
```

FIG. 30B

```
ATTATCTGAA AATTACATGA AGTATTCCAA GAGAAACCAG TATATGGATC TTGTGCTGTT   1920
CACTATGTAA ATTGTGTGAT GGTGGGTTCA GTAGTTATTG CTGTAAATGT TAGGGCAGGG   1980
CAATATGTTA CTATGAAGTT TATTGACAGT ATACTCCAAA TAGTGTTTGT GATTCAAAAG   2040
CAATATCTTT GATAGTTGGC ATTTGCAATT CCTTTATATA ATCTTTTATG AAAAAAATTG   2100
CAGAGAAAGT AAAATGTAGC TTAAAATACA GTATCCAAAA AAATGGAAAA GGGCAAACCG   2160
TGGATTAGAT AGAAATGGCA ATTCTTATAA AAAGGGTTGC ATGCTTACAT GAATGGCTTT   2220
CCATGTATAT ACTCAGTCAT TCAACAGTTT TTTTTTTAGA GCCCCATCCT TATTTTTTAT   2280
ACACTTTGAG AGCATAATGA AAAGAAAAGC TACCTGCAAA AGTTTTGGAC TTACCTCAAA   2340
GAGGATATAC TACATTCCTC AAAAGGCCTT CTTCCAGGAA TAGTATTTCA TAACCTGGAG   2400
GTTGGAAAAA TCTGGATTAG TTACAAAAAA ATCTGAGTGT TTCTAGCGGA CACAGATATT   2460
TGTCTAGGAG GGGACTAGGT TGTAGCAGTG GTAGTGCCTT ACAAGATAAA TCATGGGCTT   2520
TATTTACTTA CGAGTGGAAA AGTTGCGGAA GGTGCCTTAC AGACTTTTTT TTTGCGTTAA   2580
GTATGTGTTT TCCCATAGGA ATTAATTTAT AAATGGTGGT TTGATTTCCT CAAGTCAACC   2640
TTTAAAAGTA TATTTAGCCA AAATATAGCT TAAATATATT ACTAGTAATA AATTTAGTAC   2700
TGTGGGTCTC TCATTCTCAA AATGAGCATT TACTAATTTC TGAACACTGT GCTAGGTCCT   2760
GGGAATACCA AATTGAATAA GACATAGTCT ATTTTTCTGA AGGGTTTATA GCAGAGTCCC   2820
ATAATGAAAA AAGGAGAAGA GGGAATTC                                      2908
```